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## RAW SEQUENCE LISTING

DATE: 02/28/2002

PATENT APPLICATION: US/10/046,938

TIME: 10:24:52

Input Set : N:\Crf3\RULE60\10046938.raw.txt

Output Set: N:\CRF3\02282002\J046938.raw

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1 <110> APPLICANT: MITTAL, SURESH K.
2 GRAHAM, FRANK L.
3 PREVIC, LUDVIK
4 BABIUK, LORNE A.
5 <120> TITLE OF INVENTION: MAMMALIAN CELL LINES EXPRESSING BOVINE ADENOVIRUS FUNCTIONS
6 <130> FILE REFERENCE: 293102002102
7 <140> CURRENT APPLICATION NUMBER: 10/046,938
8 <141> CURRENT FILING DATE: 2002-01-14
10 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/435,242
W--> 11 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-05
13 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/815,927
W--> 14 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1997-03-13
15 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/164,294
W--> 16 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1993-12-09
17 <160> NUMBER OF SEQ ID NOS: 34
18 <170> SOFTWARE: PatentIn Ver. 2.0
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21 <211> LENGTH: 4060
22 <212> TYPE: DNA
23 <213> ORGANISM: Bovine adenovirus type 3
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25 <221> NAME/KEY: CDS
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34 aaattttcgg cgtcttttcc gggtttatgt ccccggtcac ctttatgact gtgtgaaaca 420
35 cacctgccca ttgttttacc ttggtcagtt ttttcgtctc ctagggtggg aacatcaaga 480
36 acaaatttgc cgaagtaattg tgcacctttt tccgcgttag gactgcgttt cacacgtaga 540
37 cagacttttt ctcattttct cacaacctgt cgtccgcttc agagctctgc gtcttcgctg 600
38 ccacc atg aag tac ctg ctc ctc gtt ctc aac gac ggc atg agt cga att 650
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40 1 5 10 15
41 gaa aaa gct ctc ctg tgc agc gat ggt gag gtg gat tta gag tgt cat 698
42 Glu Lys Ala Leu Leu Cys Ser Asp Gly Glu Val Asp Leu Glu Cys His
43 20 25 30
44 gag gta ctt ccc cct tct ccc qcg cct gtc ccc gct tct gtg tca ccc 746
45 Glu Val Leu Pro Pro Ser Pro Ala Pro Val Pro Ala Ser Val Ser Pro
46 35 40 45

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48      Val Arg Ser Pro Pro Pro Leu Ser Pro Val Phe Pro Pro Ser Pro Pro
49              50              55              60
50      gcc ccg ctt gtg aat cca gag gcg agt tcg ctg ctg cag cag tat ccg      842
51      Ala Pro Leu Val Asn Pro Glu Ala Ser Ser Leu Leu Gln Gln Tyr Arg
52              65              70              75
53      aga gag ctg tta gag agg agc ctg ctc cga acg gcc gaa ggt cag cag      890
54      Arg Glu Leu Leu Glu Arg Ser Leu Leu Arg Thr Ala Glu Gly Gln Gln
55              80              85              90              95
56      cgt gca gtg tgt cca tgt gag ccg ttg ccc gtg gaa gag gat gag tgt      938
57      Arg Ala Val Cys Pro Cys Glu Arg Leu Pro Val Glu Glu Asp Glu Cys
58              100              105              110
59      ctg aat gcc gta aat ttg ctg ttt cct gat ccc tgg cta aat gca gct      986
60      Leu Asn Ala Val Asn Leu Leu Phe Pro Asp Pro Trp Leu Asn Ala Ala
61              115              120              125
62      gaa aat ggg ggt gat att ttt aag tct ccg gct atg tct cca gaa ccg      1034
63      Glu Asn Gly Gly Asp Ile Phe Lys Ser Pro Ala Met Ser Pro Glu Pro
64              130              135              140
65      tgg ata gat ttg tct agc tac gat agc gat gta gaa gag gtg act agt      1082
66      Trp Ile Asp Leu Ser Ser Tyr Asp Ser Asp Val Glu Glu Val Thr Ser
67              145              150              155
68      cac ttt ttt ctg gat tgc cct gaa gac ccc agt ccg gag tgt tca tct      1130
69      His Phe Phe Leu Asp Cys Pro Glu Asp Pro Ser Arg Glu Cys Ser Ser
70              160              165              170              175
71      tgt ggg ttt cat cag gct caa agc gga att cca ggc att atg tgc agt      1178
72      Cys Gly Phe His Gln Ala Gln Ser Gly Ile Pro Gly Ile Met Cys Ser
73              180              185              190
74      ttg tgc tac atg cgc caa acc tac cat tgc atc tat agtaagtaca      1224
75      Leu Cys Tyr Met Arg Gln Thr Tyr His Cys Ile Tyr
76              195              200
77      ttctgtaaaa gaacatcttg gtgatttota ggtattgttt agggattaac tgggtggagt      1284
78      gatcttaate ccgcataacc aaatacatgt ttccacag gt cca gtt tct gaa gag      1339
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81      gaa atg tgagtcagt tgactttggc gcgcaagagg aaatgtgagt catgttgact      1395
82      Glu Met
83      210
84      ttggcgcgcc ctacggtgac tttaaagcaa tttagaggatc acttttttgt tagtcgctat      1455
85      aaagtagtca ccgagctctc atggatcact taagcgttct tttggatttg aagctgcttc      1515
86      gctctatcgt agcgggggct tcaaatcgca ctggagtgtg gaagagccgg ctgtggctgg      1575
87      qacgcctgac tcaactggtc catgatacct gcgtagagaa cgagagcata ttctcaatt      1635
88      ctctgccagg gaatgaagct tttttaagggt tgcttcggag ccgctatttt gaagtgtttg      1695
89      acgtgtttgt ggtgcctgag ctgcactctg acactccggg tcgagtggtc gccgctcttg      1755
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92      tcaccagag ctccaggagc acttcgcagc ctctctctgc gcccgacaag acgaccaga      1935
93      ctaccagcca gttagacggg acagccaccc cggggctagc ctggaggagg ctgaacagag      1995
94      cagactcgt ttcgagcaca tcagttaccg agacgtggtg gatgacttca atagatgcca      2055
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98  tactattagg gtaacagggg aagcctcccc ggcatttaga gtgggggcca tggcctggg 2295
99  tccgtgtgta acaggaatga ctgggggtgac ttttgtgaat tgtaggtttg agagagagtc 2355
100  aacaattagg ggtccctga taagagcttc aactcacgtg ctgtttcatg gctgttattt 2415
101  tatgggaatt atgggcactt gtattgaggt gggggcggga gcttacatc ggggttgtga 2475
102  gtttgtgggc tgttacggg gaactctgtt tacttctaac agagatatta aggtgaggca 2535
103  gtgcaacttt gacaaatgct tactgggtat tacttgtaag ggggactatc gtctttcggg 2595
104  aaatgtgtgt tctgagactt tctgctttgc tcatcttagag ggagaggggt tggttaaaaa 2655
105  caacacagtc aagtcacctt gtcgctggac cagcaggtct ggtctttcca tgataacttg 2715
106  tgcagacggc aggtttaagc ctctgggttc cctccacatt gtgggcaacc gttgtagcgc 2775
107  ttggccaacc atgcagggga atgtgtttat catgtctaaa ctgtatctgg gcaacagaat 2835
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109  ggcgacaaac aagctggtct tggcttgtgc ttttgagaat aatgtactgg tgtacaaagt 2955
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111  aaagcctttg aacttgcaa ttatttcttc agatattcgg gctaactgat acatgtacac 3075
112  tgtggactca acagagttca ctctgacga ggattaaaag tgggcggggc caagaggggt 3135
113  ataaataggt ggggaggttg aggggagcgc tagttctctg ttttccaga ctggggggga 3195
114  caacatggcc gaggaagggc gcatttatgt gctttatgta actgcccgc tgcccaagtg 3255
115  gtcgggttcg gtgcagata agcgggctc gaacatgttg gggggtgtgg tactccctcc 3315
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125  ggggtgattg caaaggaggt ctcttagtgt aggtattgat aaatctgttc agttgggagg 3915
126  gatgcattcg ggggctaata aggtggaggt tagcctgaat cttaaggttg gcaatgttgc 3975
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130 &lt;210&gt; SEQ ID NO: 2

131 &lt;211&gt; LENGTH: 211

132 &lt;212&gt; TYPE: PRT

133 &lt;213&gt; ORGANISM: Bovine adenovirus type 3

134 &lt;400&gt; SEQUENCE: 2

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135  Met Lys Tyr Leu Val Leu Val Leu Asn Asp Gly Met Ser Arg Ile Glu
136      1              5              10              15
137  Lys Ala Leu Leu Cys Ser Asp Gly Glu Val Asp Leu Glu Cys His Glu
138      20              25              30
139  Val Leu Pro Pro Ser Pro Ala Pro Val Pro Ala Ser Val Ser Pro Val
140      35              40              45
141  Arg Ser Pro Pro Pro Leu Ser Pro Val Phe Pro Pro Ser Pro Pro Ala
142      50              55              60
143  Pro Leu Val Asn Pro Glu Ala Ser Ser Leu Leu Gln Gln Tyr Arg Arg
144      65              70              75              80
145  Glu Leu Leu Glu Arg Ser Leu Leu Arg Thr Ala Glu Gly Gln Gln Arg

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147   Ala Val Cys Pro Cys Glu Arg Leu Pro Val Glu Glu Asp Glu Cys Leu
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149   Asn Ala Val Asn Leu Leu Phe Pro Asp Pro Trp Leu Asn Ala Ala Glu
150                               115                               120                               125
151   Asn Gly Gly Asp Ile Phe Lys Ser Pro Ala Met Ser Pro Glu Pro Trp
152                               130                               135                               140
153   Ile Asp Leu Ser Ser Tyr Asp Ser Asp Val Glu Glu Val Thr Ser His
154                               145                               150                               155                               160
155   Phe Phe Leu Asp Cys Pro Glu Asp Pro Ser Arg Glu Cys Ser Ser Cys
156                               165                               170                               175
157   Gly Phe His Gln Ala Gln Ser Gly Ile Pro Gly Ile Met Cys Ser Leu
158                               180                               185                               190
159   Cys Tyr Met Arg Gln Thr Tyr His Cys Ile Tyr Ser Pro Val Ser Glu
160                               195                               200                               205
161   Glu Glu Met
162                               210
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167 <213> ORGANISM: Bovine adenovirus type 3
168 <220> FEATURE:
169 <221> NAME/KEY: CDS
170 <222> LOCATION: (1476)..(1946)
171 <400> SEQUENCE: 3
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174   cgtcgcggag gcggcgggcg tggcgggggc tgagggcggc gggggcggcg cgcgggcgcg 180
175   cgcgcggggc gggcgagagg gcgaggttcc gcaccgccta cgtcattttc agacattttt 240
176   tagcaaatat gcgccttttg caagcatttt tctcacattt caggtattta gagggcggat 300
177   ttttggtgtt cgtacttccg tgtcacatag ttcactgtca atcttcatta cggttagaac 360
178   aaattttcgg cgtcttttcc gggtttatgt ccccggtcac ctttatgact gtgtgaaaca 420
179   cacctgccca ttgtttaccc ttggtcagtt ttttcgtctc ctagggtggg aacatcaaga 480
180   acaaatttgc cgagtaattg tgcacctttt tccgcgttag gactgcgttt cacacgtaga 540
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186   ggagagagct gttagagagg agcctgctcc gaacggccga aggtcagcag cgtgcagtgt 900
187   gtccatgtga gcggttgccc gtggaagagg atgagtgtct gaatgccgta aatttgctgt 960
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189   tgtctccaga accgtggata gatttgtcta gctacgatag cgatgtagaa gaggtgacta 1080
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191   atcaggetca aagcgggaatt ccaggcatta tgtgcagttt gtgctacatg cgcctaacct 1200
192   accattgcat ctatagtaag tacattctgt aaaagaacat cttggtgatt tctaggtatt 1260
193   qtttagggat taactgggtg gagtgtatct aatccggcat aaccataaac atgttttcac 1320
194   aggtccagtt tctgaagagg aaatgtgagt catgttgact ttggcgcgca agaggaaatg 1380
195   tqagtcagtg tgactttggc gcqccctaag gtgactttaa agcaatttga gqatcacttt 1440

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198                                     1           5
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200   Leu Leu Asp Leu Lys Leu Leu Arg Ser Ile Val Ala Gly Ala Ser Asn
201               10           15           20
202   cgc act gga gtg tgg aag agg cgg ctg tgg ctg gga cgc ctg act caa   1589
203   Arg Thr Gly Val Trp Lys Arg Arg Leu Trp Leu Gly Arg Leu Thr Gln
204               25           30           35
205   ctg gtc cat gat acc tgc gta gag aac gag agc ata ttt ctc aat tct   1637
206   Leu Val His Asp Thr Cys Val Glu Asn Glu Ser Ile Phe Leu Asn Ser
207               40           45           50
208   ctg cca ggg aat gaa gct ttt tta agg ttg ctt cgg agc ggc tat ttt   1685
209   Leu Pro Gly Asn Glu Ala Phe Leu Arg Leu Leu Arg Ser Gly Tyr Phe
210               55           60           65           70
211   gaa gtg ttt gac gtg ttt gtg gtg cct gag ctg cat ctg gac act ccg   1733
212   Glu Val Phe Asp Val Phe Val Val Pro Glu Leu His Leu Asp Thr Pro
213               75           80           85
214   ggt cga gtg gtc gcc gct ctt gct ctg ctg gtg ttc atc ctc aac gat   1781
215   Gly Arg Val Val Ala Ala Leu Ala Leu Leu Val Phe Ile Leu Asn Asp
216               90           95           100
217   tta gac gct aat tct gct tct tca ggc ttt gat tca ggt ttt ctc gtg   1829
218   Leu Asp Ala Asn Ser Ala Ser Ser Gly Phe Asp Ser Gly Phe Leu Val
219               105           110           115
220   gac cgt ctc tgc gtg ccg cta tgg ctg aag gcc agg gcg ttc aag atc   1877
221   Asp Arg Leu Cys Val Pro Leu Trp Leu Lys Ala Arg Ala Phe Lys Ile
222               120           125           130
223   acc cag agc tcc agg agc act tcg cag cct tcc tcg tcg ccc gac aag   1925
224   Thr Gln Ser Ser Arg Ser Thr Ser Gln Pro Ser Ser Ser Pro Asp Lys
225               135           140           145           150
226   acg acc cag act acc agc cag tagacgggga cagcccaccc cgggctagcc   1976
227   Thr Thr Gln Thr Thr Ser Gln
228               155
229   tggaggaggc tgaacagagc agcactcggt tcgagcacat cagttaccga gacgtggtgg   2036
230   atgaactcaa taqatgcoat gatgtttttt atgagaggta cagttttgag gacataaaga   2096
231   gctacgaggc ttgcctgag gacaatttgg agcagctcat agctatgcat gctaaaatca   2156
232   agctgctgcc ccgtcgggag tatgagttga ctcaaccttt gaacataaca tcttgcgcct   2216
233   atgtgctcgg aaatggggct actattaggg taacagggga agcctccccg gctattagag   2276
234   tgggggccat ggcctgqggg ccgtgtgtaa caggaatgac tggggtgact tttgtgaatt   2336
235   gtaggtttga gagagagtea acaattaggg ggtccctgat acgagcttca actcacgtgc   2396
236   tgtttcatgg ctgttatttt atgggaatta tgggcacttg tattgaggtg ggggcgggag   2456
237   cttacattcg gggttggtgag tttgtgggct gttaccgggg aatctgttct acttctaaac   2516
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239   gggactatcg tctttcggga aatgtgtgtt ctgagacttt ctgctttgct catttaagag   2636
240   gagagggttt ggttaaaaaa aacacagtea agtcccctag tcgctggacc agcaggtctg   2696
241   gcttttccat gataacttgt gcagacggga gggttacgcc tttgggttcc ctccacattg   2756
242   tgggcaaccg ttgtaggcgt tggccaacca tgcaggggaa tgtgtttatc atgtctaaac   2816
243   gtatctggg caacagaata gggactgtag cctgccecca gtgtgcttcc tacaagtcca   2876
244   gcatttqttt qgaggagagg qcgacaaaca agctggtctt ggcttgtgct tttgagaata   2936

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L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:26 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:1, CDS LOCATION: join  
(606..1215, 1323..1345)  
L:39 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 1, CDS LOCATION:0..606  
L:79 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 1  
L:1961 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30  
L:1963 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30  
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L:1969 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
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